

#2

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,104
Source: PCT
Date Processed by STIC: 3-25-05

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[Handwritten scribbles and marks in the bottom left corner]



PCT

RAW SEQUENCE LISTING

DATE: 03/25/2005

PATENT APPLICATION: US/10/528,104

TIME: 09:22:35

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03252005\J528104.raw

3 <110> APPLICANT: G2M Cancer Drugs AG
 4 Forschungszentrum Karlsruhe GmbH
 6 <120> TITLE OF INVENTION: The use of molecular markers for the preclinical and
 clinical profiling
 7 of inhibitors of enzymes having histone deacetylase activity
 9 <130> FILE REFERENCE: molecular markers
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/528,104
 C--> 11 <141> CURRENT FILING DATE: 2005-03-16
 11 <160> NUMBER OF SEQ ID NOS: 8
 13 <170> SOFTWARE: PatentIn version 3.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 488
 17 <212> TYPE: PRT
 18 <213> ORGANISM: homo sapiens
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 23 1 5 10 15
 26 Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro Met Lys
 27 20 25 30
 30 Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr Gly Leu
 31 35 40 45
 34 Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr Ala Glu Glu
 35 50 55 60
 38 Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu Arg Ser Ile
 39 65 70 75 80
 42 Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met His Ile Phe Asn
 43 85 90 95
 46 Val Gly Glu Asp Cys Pro Ala Phe Asp Gly Leu Phe Glu Phe Cys Gln
 47 100 105 110
 50 Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu Asn Arg Gln
 51 115 120 125
 54 Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys
 55 130 135 140
 58 Lys Tyr Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala
 59 145 150 155 160
 62 Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile
 63 165 170 175
 66 Asp Ile His His Gly Asp Gly Val Glu Ala Phe Tyr Thr Thr Asp
 67 180 185 190
 70 Arg Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly
 71 195 200 205
 74 Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala
 75 210 215 220
 78 Val Asn Phe Pro Met Cys Asp Gly Ile Asp Asp Glu Ser Tyr Gly Gln

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79 225                230                235                240
82 Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr Gln Pro Ser,
83                245                250                255
86 Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp Arg Leu
87                260                265                270
90 Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys Val Glu Val
91                275                280                285
94 Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly Gly Tyr
95                290                295                300
98 Thr Ile Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala
99 305                310                315                320
102 Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu
103                325                330                335
106 Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr
107                340                345                350
110 Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln Arg Leu Phe
111                355                360                365
114 Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala
115                370                375                380
118 Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu Asp Gly Glu
119 385                390                395                400
122 Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys Arg Ile Ala
123                405                410                415
126 Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu Gly Arg
127                420                425                430
130 Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Lys Ala Arg Ile Glu
131                435                440                445
134 Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val Lys Glu Glu
135                450                455                460
138 Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr Lys Gly Thr
139 465                470                475                480
142 Lys Ser Glu Gln Leu Ser Asn Pro
143                485
146 <210> SEQ ID NO: 2
147 <211> LENGTH: 183
148 <212> TYPE: PRT
149 <213> ORGANISM: homo sapiens
151 <400> SEQUENCE: 2
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157 Lys Leu Ile Glu Ser Lys His Glu Val Thr Ile Leu Gly Gly Leu Asn
158                20                25                30
161 Glu Phe Val Val Lys Phe Tyr Gly Pro Gln Gly Thr Pro Tyr Glu Gly
162                35                40                45
165 Gly Val Trp Lys Val Arg Val Asp Leu Pro Asp Lys Tyr Pro Phe Lys
166                50                55                60
169 Ser Pro Ser Ile Gly Phe Met Asn Lys Ile Phe His Pro Asn Ile Asp
170 65                70                75                80
173 Glu Ala Ser Gly Thr Val Cys Leu Asp Val Ile Asn Gln Thr Trp Thr

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174      85      90      95
177 Ala Leu Tyr Asp Leu Thr Asn Ile Phe Glu Ser Phe Leu Pro Gln Leu
178      100      105      110
181 Leu Ala Tyr Pro Asn Pro Ile Asp Pro Leu Asn Gly Asp Ala Ala Ala
182      115      120      125
185 Met Tyr Leu His Arg Pro Glu Glu Tyr Lys Gln Lys Ile Lys Glu Tyr
186      130      135      140
189 Ile Gln Lys Tyr Ala Thr Glu Glu Ala Leu Lys Glu Gln Glu Glu Gly
190 145      150      155      160
193 Thr Gly Asp Ser Ser Glu Ser Ser Met Ser Asp Phe Ser Glu Asp
194      165      170      175
197 Glu Ala Gln Asp Met Glu Leu
198      180
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 624
203 <212> TYPE: PRT
204 <213> ORGANISM: homo sapiens
206 <400> SEQUENCE: 3
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209 1      5      10      15
212 Ala Gln Arg Arg Ser Gln Met Asp Arg Leu Asp Arg Glu Glu Ala Phe
213      20      25      30
216 Tyr Gln Phe Val Asn Asn Leu Ser Glu Glu Asp Tyr Arg Leu Met Arg
217      35      40      45
220 Asp Asn Asn Leu Leu Gly Thr Pro Gly Glu Ser Thr Glu Glu Glu Leu
221      50      55      60
224 Leu Arg Arg Arg Leu Gln Gln Ile Lys Glu Gly Pro Pro Gln Asn Ser
225 65      70      75      80
228 Asp Glu Asn Arg Gly Gly Asp Ser Ser Asp Asp Val Ser Asn Gly Asp
229      85      90      95
232 Ser Ile Ile Asp Trp Leu Asn Ser Val Arg Gln Thr Gly Asn Thr Thr
233      100      105      110
236 Arg Ser Gly Gln Arg Gly Asn Gln Ser Trp Arg Ala Val Cys Arg Thr
237      115      120      125
240 Asn Pro Asn Ser Gly Asn Phe Arg Phe Ser Leu Glu Ile Asn Val Tyr
241      130      135      140
244 Ser Asn Asn Gly Ser Gln Asn Ser Glu Asn Glu Asn Glu Pro Ser Ala
245 145      150      155      160
248 Arg Arg Ser Ser Gly Glu Asn Val Glu Asn Asn Ser Gln Arg Gln Val
249      165      170      175
252 Glu Asn Pro Arg Ser Glu Ser Thr Ser Ala Arg Pro Ser Arg Ser Glu
253      180      185      190
256 Arg Asn Ser Thr Glu Ala Leu Thr Glu Val Pro Pro Thr Arg Gly Gln
257      195      200      205
260 Arg Arg Ala Arg Ser Arg Ser Pro Asp His Arg Arg Thr Arg Ala Arg
261      210      215      220
264 Ala Glu Arg Ser Arg Ser Pro Leu His Pro Met Ser Glu Ile Pro Arg
265 225      230      235      240
268 Arg Ser His His Ser Ile Ser Ser Gln Thr Phe Glu His Pro Leu Val

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269          245          250          255
272 Asn Glu Thr Glu Gly Ser Ser Arg Thr Arg His His Val Thr Leu Arg
273          260          265          270
276 Gln Gln Ile Ser Gly Pro Glu Leu Leu Ser Arg Gly Leu Phe Ala Ala
277          275          280          285
280 Ser Gly Thr Arg Asn Ala Ser Gln Gly Ala Gly Ser Ser Asp Thr Ala
281          290          295          300
284 Ala Ser Gly Glu Ser Thr Gly Ser Gly Gln Arg Pro Pro Thr Ile Val
285 305          310          315          320
288 Leu Asp Leu Gln Val Arg Arg Val Arg Pro Gly Glu Tyr Arg Gln Arg
289          325          330          335
292 Asp Ser Ile Ala Ser Arg Thr Arg Ser Arg Ser Gln Thr Pro Asn Asn
293          340          345          350
296 Thr Val Thr Tyr Glu Ser Glu Arg Gly Gly Phe Arg Arg Thr Phe Ser
297          355          360          365
300 Arg Ser Glu Arg Ala Gly Val Arg Thr Tyr Val Ser Thr Ile Arg Ile
301          370          375          380
304 Pro Ile Arg Arg Ile Leu Asn Thr Gly Leu Ser Glu Thr Thr Ser Val
305 385          390          395          400
308 Ala Ile Gln Thr Met Leu Arg Gln Ile Met Thr Gly Phe Gly Glu Leu
309          405          410          415
312 Ser Tyr Phe Met Tyr Ser Asp Ser Asp Ser Glu Pro Thr Gly Ser Val
313          420          425          430
316 Ser Asn Arg Asn Met Glu Arg Ala Glu Ser Arg Ser Gly Arg Gly Gly
317          435          440          445
320 Ser Gly Gly Gly Ser Ser Ser Gly Ser Ser Ser Ser Ser Ser Ser
321          450          455          460
324 Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Ser Ser Ser
325 465          470          475          480
328 Ser Gly Gly Glu Ser Ser Glu Thr Ser Ser Asp Leu Phe Glu Gly Ser
329          485          490          495
332 Asn Glu Gly Ser Ser Ser Ser Gly Ser Ser Gly Ala Arg Arg Glu Gly
333          500          505          510
336 Arg His Arg Ala Pro Val Thr Phe Asp Glu Ser Gly Ser Leu Pro Phe
337          515          520          525
340 Leu Ser Leu Ala Gln Phe Phe Leu Leu Asn Glu Asp Asp Asp Asp Gln
341          530          535          540
344 Pro Arg Gly Leu Thr Lys Glu Gln Ile Asp Asn Leu Ala Met Arg Ser
345 545          550          555          560
348 Phe Gly Glu Asn Asp Ala Leu Lys Thr Cys Ser Val Cys Ile Thr Glu
349          565          570          575
352 Tyr Thr Glu Gly Asn Lys Leu Arg Lys Leu Pro Cys Ser His Glu Tyr
353          580          585          590
356 His Val His Cys Ile Asp Arg Trp Leu Ser Glu Asn Ser Thr Cys Pro
357          595          600          605
360 Ile Cys Arg Arg Ala Val Leu Ala Ser Gly Asn Arg Glu Ser Val Val
361          610          615          620
364 <210> SEQ ID NO: 4
365 <211> LENGTH: 281

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366 <212> TYPE: PRT
367 <213> ORGANISM: homo sapiens
369 <400> SEQUENCE: 4
371 Met Ala Met Met Glu Val Gln Gly Gly Pro Ser Leu Gly Gln Thr Cys
372 1 5 10 15
375 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala
376 20 25 30
379 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys
380 35 40 45
383 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr
384 50 55 60
387 Trp Asp Pro Asn Asp Glu Ser Met Asn Ser Pro Cys Trp Gln Val
388 65 70 75 80
391 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser
392 85 90 95
395 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro
396 100 105 110
399 Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr Gly
400 115 120 125
403 Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn Glu
404 130 135 140
407 Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser Gly
408 145 150 155 160
411 His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val Ile
412 165 170 175
415 His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg Phe
416 180 185 190
419 Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val Gln
420 195 200 205
423 Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met Lys
424 210 215 220
427 Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu Tyr
428 225 230 235 240
431 Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg Ile
432 245 250 255
435 Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
436 260 265 270
439 Ser Phe Phe Gly Ala Phe Leu Val Gly
440 275 280

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443 <210> SEQ ID NO: 5

444 <211> LENGTH: 1985

445 <212> TYPE: DNA

446 <213> ORGANISM: homo sapiens

448 <400> SEQUENCE: 5

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449 cgccgagctt tcggcacctc tgccgggtgg taccgagcct tcccggcgcc cctcctctc 60
451 ctcccaccgg cctgcccttc ccgcgggac tatcgcccc acgtttccct cagccctttt 120
453 ctctcccggc cgagccgcgg cggcagcagc agcagcagca gcagcaggag gaggagcccg 180
455 gtggcgggcg tggcggggga gcccatggcg tacagtcaag gaggcggcaa aaaaaaagtc 240
457 tgctactact acgacgggtga tattggaaat tattattatg gacaggggtca tcccatgaag 300

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VERIFICATION SUMMARY

DATE: 03/25/2005

PATENT APPLICATION: US/10/528,104

TIME: 09:22:36

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03252005\J528104.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date